

ABSTRACT

Relatedness between genes is quantified by constructing nonlinear models predicting gene expression. Effectiveness of the model is evaluated to provide a measurement of the relatedness of genes associated with the model. Various types of models, including full-logic or neural networks can be constructed. A graphical user interface presents results of the analysis to allow evaluation by a user. Each gene's contribution to the measurement of relatedness can be shown on a graph, and graphical representations of models used to predict gene expression can be displayed.

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